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☐ **Q9NX09**. Reports DNA-damage-induci...[gi:74753036]

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LOCUS Q9NX09 232 aa linear PRI 13-NOV-2007
DEFINITION DNA-damage-inducible transcript 4 protein (Protein regulated in development and DNA damage response 1) (REDD-1) (HIF-1 responsive protein RTP801).
ACCESSION Q9NX09
VERSION Q9NX09.1 GI:74753036
DBSOURCE swissprot: locus DDT4_HUMAN, accession [Q9NX09](#); class: standard.
 extra accessions: Q9H0S3
 created: Oct 23, 2007.
 sequence updated: Oct 1, 2000.
 annotation updated: Nov 13, 2007.
 xrefs: AY090097.1, AAM10442.1, AF335324.1, AAL38424.1, AK000507.1, BAA91214.1, AL136668.1, CAB56603.1, AL683820.13, CAH73863.1, CH471083.1, EAW54452.1, BC020708.1, [AAH0C708.1](#), [BC007714.1](#), [AAH07714.1](#), [BC015236.1](#), [AAH15236.1](#)
 xrefs (non-sequence databases): RefSeq:NP_061931.1, UniGene:Hs.5230.2, Ensembl:ENSG00000168209, GeneID:54541, KEGG:hsa:54541, HGNC:24944, MIM:607729, PharmGKB:PA134977994, ArrayExpress:Q9NX09, InterPro:IPR012918, PANTHER:PTHR12478, Pfam:PF07809
KEYWORDS Apoptosis; Cytoplasm.
SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
[Eukaryota](#); [Metazoa](#); [Chordata](#); [Craniata](#); [Vertebrata](#); [Euteleostomi](#); [Mammalia](#); [Eutheria](#); [Euarchontoglires](#); [Primates](#); [Haplorrhini](#); [Catarrhini](#); [Hominidae](#); [Homo](#).
REFERENCE 1 (residues 1 to 232)
AUTHORS Ellisen,L.W., Ramsayer,K.D., Johannessen,C.M., Yang,A., Beppu,H., Minda,K., Oliner,J.D., McKeon,F. and Haber,D.A.
TITLE REDD1, a developmentally regulated transcriptional target of p63 and p53, links p63 to regulation of reactive oxygen species
JOURNAL Mol. Cell 10 (5), 995-1005 (2002)
PUBMED 12453409
REMARK NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, INDUCTION BY DNA DAMAGE, AND SUBCELLULAR LOCATION.
 TISSUE=Petal brain
REFERENCE 2 (residues 1 to 232)
AUTHORS Shoshani,T., Faerman,A., Mett,I., Zelin,E., Tenne,T., Gorodin,S., Moshel,Y., Elbaz,S., Budanov,A., Chajut,A., Kalinski,H., Kamer,I., Rozen,A., Mor,O., Keshet,E., Leshkowitz,D., Einat,P., Skalter,R. and Feinstein,E.
TITLE Identification of a novel hypoxia-inducible factor 1-responsive gene, RTP801, involved in apoptosis
JOURNAL Mol. Cell. Biol. 22 (7), 2283-2293 (2002)
PUBMED 11884613
REMARK NUCLEOTIDE SEQUENCE [MRNA], TISSUE SPECIFICITY, AND INDUCTION.
REFERENCE 3 (residues 1 to 232)

AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Ohayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahara,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T.O., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Miasashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiya,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigetani,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano.S

TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)

PUBMED 14702039

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] .

REFERENCE 4 (residues 1 to 232)

CONSTRM The German cDNA consortium

TITLE Direct Submission

JOURNAL Submitted (??-SEP-2004)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] .

TISSUE Brain

REFERENCE 5 (residues 1 to 232)

AUTHORS Mural,R.J., Istrail,S., Sutton,G.G., Florea,L., Halpern,A.L., Mobarry,C.M., Lippert,R., Walenz,B., Shatkay,H., Dew,I., Miller,J.R., Flanigan,M.J., Edwards,N.J., Bolanos,R., Fasulo,D., Halldorsson,B.V., Hancherhalli,S., Turner,R., Yooseph,S., Lu,F., Nusskern,D.R., Shue,B.C., Zheng,X.H., Zhong,F., Delcher,A.L., Huson,D.H., Kravitz,S.A., Mouchard,L., Reinert,K., Remington,K.A., Clark,A.G., Waterman,M.S., Eichler,E.E., Adams,M.D., Hunkapiller,M.W., Myers,E.W. and Venter,J.C.

TITLE Direct Submission

JOURNAL Submitted (??-JUL-2005)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] .

REFERENCE 6 (residues 1 to 232)

AUTHORS Deloukas,P., Earthworm,M.E., Grafham,D.V., Rubinfeld,M., French,L., Steward,C.A., Sims,S.K., Jones,M.C., Searle,S., Scott,C., Howe,K., Hunt,S.E., Andrews,T.D., Gilbert,J.G., Swarbreck,D., Ashurst,J.L., Taylor,A., Battles,J., Bird,C.P., Ainscough,R., Almeida,J.P., Ashwell,R.I., Ambrose,K.D., Babbage,A.K., Bagguley,C.L., Bailey,J., Banerjee,R., Bates,K., Beasley,H., Bray-Allen,S., Brown,A.J., Brown,J.Y., Burford,D.C., Burrill,W., Burton,J., Cahill,P., Camire,D., Carter,N.P., Chapman,J.C., Clark,S.Y., Clarke,G., Clee,C.M., Clegg,S., Corby,N., Coulson,A., Dhami,P., Dutta,I., Dunn,M., Faulkner,L., Frankish,A., Frankland,J.A., Garner,P., Garnett,J., Gribble,S., Griffiths,C., Grocock,R., Gustafson,E., Hammond,S., Harley,J.L., Hart,E., Heath,P.D., Ho,T.P., Hopkins,B., Horne,J., Howden,P.J., Huckle,E., Hynds,C., Johnson,C., Johnson,D., Kana,A., Kay,M., Kimberley,A.M., Kershaw,J.K., Kokkinaki,M., Laird,G.K., Lawlor,S., Lee,H.M.,

Leongamornlert,D.A., Laird,G., Lloyd,C., Lloyd,D.M., Loveland,J., Lovell,J., McLaren,S., McLay,K.E., McMurray,A., Mashreghi-Mohammadi,M., Matthews,L., Milne,S., Nickerson,T., Nguyen,M., Overton-Larty,E., Palmer,S.A., Pearce,A.V., Peck,A.I., Pelan,S., Phillimore,B., Porter,K., Rice,C.M., Rogosin,A., Ross,M.T., Sarafidou,T., Sehra,H.K., Shownkeen,R., Skuce,C.D., Smith,M., Standring,L., Sycamore,N., Tester,J., Thorpe,A., Torcasso,W., Tracey,A., Tromans,A., Tsolas,J., Wall,M., Walsh,J., Wang,H., Weinstock,K., West,A.P., Willey,D.L., Whitehead,S.L., Wilming,L., Wray,P.W., Young,L., Chen,Y., Lovering,R.C., Moschonas,N.K., Siebert,R., Fecitel,K., Bentley,D., Durbin,R., Hubbard,T., Doucette-Stamm,L., Beck,S., Smith,D.R. and Rogers,J. The DNA sequence and comparative analysis of human chromosome 10 Nature 429 (6990), 375-381 (2004)

TITLE
JOURNAL
PUBMED
REMARK
REFERENCE
AUTHORS

15164054
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
7 (residues 1 to 232)
Gerhard,D.S., Wagner,L., Feingold,E.A., Shenmen,C.M., Grouse,L.H., Schuler,G., Klein,S.L., Old,S., Rasooly,R., Good,P., Guyer,M., Peck,A.M., Derge,J.G., Lipman,D., Collins,F.S., Jang,W., Sherry,S., Feolo,M., Misquitta,L., Lee,E., Rotmistrovsky,K., Greenhut,S.F., Schaefer,C.F., Buetow,K., Bonner,T.I., Haussler,D., Kent,J., Kiekhaus,M., Furey,T., Brent,M., Prange,C., Schreiber,K., Shapiro,N., Bhat,N.K., Hopkins,R.F., Hsie,F., Driscoll,T., Soares,M.B., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S., Carninci,P., Piao,Y., Dudekula,D.B., Ko,M.S., Kawakami,K., Suzuki,Y., Sugano,S., Gruber,C.E., Smith,M.R., Simmons,B., Moore,T., Waterman,R., Johnson,S.L., Ruan,Y., Wei,C.L., Mathavan,S., Gunaratne,P.H., Wu,J., Garcia,A.M., Hulyk,S.W., Fuh,E., Yuan,Y., Sneed,A., Kowis,C., Hodgson,A., Muzny,D.M., McPherson,J., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madari,A., Young,A.C., Wetherby,K.D., Granite,S.J., Kwong,P.N., Brinkley,C.P., Pearson,R.L., Bouffard,G.G., Blakesley,R.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Griffith,M., Griffith,O.L., Krzywinski,M.I., Liao,N., Morin,R., Palmquist,D., Petrescu,A.S., Skalska,U., Smailus,D.E., Stott,J.M., Schnerch,A., Schein,J.E., Jones,S.J., Holt,R.A., Baross,A., Marra,M.A., Clifton,S., Makowski,K.A., Bosak,S. and Malek,J.

CONSTRM
TITLE
JOURNAL
PUBMED
REMARK
REFERENCE
AUTHORS

MGC Project Team
The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC)
Genome Res. 14 (10B), 2121-2127 (2004)
15489334
NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
TISSUE=Kidney, and Uterus
Erratum:[Genome Res. 2006 Jun;16(6):804. Morrin, Ryan [corrected to Morin, Ryan]]
8 (residues 1 to 232)
Kim,J.R., Lee,S.R., Chung,H.J., Kim,S., Baek,S.H., Kim,J.H. and Kim,Y.S.

TITLE
JOURNAL
PUBMED
REMARK
REFERENCE
AUTHORS

Identification of amyloid beta-peptide responsive genes by cDNA microarray technology: involvement of RTP801 in amyloid beta-peptide toxicity
Exp. Mol. Med. 35 (5), 403-411 (2003)
14646594
INDUCTION.
9 (residues 1 to 232)
Brugarolas,J., Lei,K., Hurler,R.L., Manning,B.D., Reiling,J.H., Hafen,E., Witters,L.A., Ellisen,L.W. and Kaelin,W.G. Jr.

TITLE
JOURNAL
PUBMED
REMARK
REFERENCE
AUTHORS

Regulation of mTOR function in response to hypoxia by REDD1 and the TSC1/TSC2 tumor suppressor complex
Genes Dev. 18 (23), 2893-2904 (2004)
15545625
FUNCTION.
10 (residues 1 to 232)
Lin,L., Qian,Y., Shi,X. and Chen,Y.

TITLE Induction of a cell stress response gene RTP801 by DNA damaging agent methyl methanesulfonate through CCAAT/enhancer binding protein

JOURNAL Biochemistry 44 (10), 3909-3914 (2005)

PUBMED 15751966

REMARK INDUCTION.

REFERENCE 11 (residues 1 to 232)

AUTHORS Corradetti,M.N., Inoki,K. and Guan,K.L.

TITLE The stress-induced proteins RTP801 and RTP801L are negative regulators of the mammalian target of rapamycin pathway

JOURNAL J. Biol. Chem. 280 (11), 9769-9772 (2005)

PUBMED 15632201

REMARK FUNCTION.

REFERENCE 12 (residues 1 to 232)

AUTHORS Sofer,A., Lei,K., Johannessen,C.M. and Ellisen,L.W.

TITLE Regulation of mTOR and cell growth in response to energy stress by REDD1

JOURNAL Mol. Cell. Biol. 25 (14), 5834-5845 (2005)

PUBMED 15988001

REMARK FUNCTION.

REFERENCE 13 (residues 1 to 232)

AUTHORS Schwarzer,R., Tondera,D., Arnold,W., Giese,K., Klippel,A. and Kaufmann,J.

TITLE REDD1 integrates hypoxia-mediated survival signaling downstream of phosphatidylinositol 3-kinase

JOURNAL Oncogene 24 (7), 1138-1149 (2005)

PUBMED 15592522

REMARK INDUCTION.

REFERENCE 14 (residues 1 to 232)

AUTHORS Malagelada,C., Ryu,E.J., Biswas,S.C., Jackson-Lewis,V. and Greene,L.A.

TITLE RTP801 is elevated in Parkinson brain substantia nigral neurons and mediates death in cellular models of Parkinson's disease by a mechanism involving mammalian target of rapamycin inactivation

JOURNAL J. Neurosci. 26 (39), 9996-10005 (2006)

PUBMED 17005863

REMARK FUNCTION, AND TISSUE SPECIFICITY.

REFERENCE 15 (residues 1 to 232)

AUTHORS Gery,S., Park,D.J., Vuong,P.T., Virk,R.K., Muller,C.I., Hofmann,W.K. and Koeffler,H.P.

TITLE RTP801 is a novel retinoic acid-responsive gene associated with myeloid differentiation

JOURNAL Exp. Hematol. 35 (4), 572-578 (2007)

PUBMED 17379067

REMARK FUNCTION, TISSUE SPECIFICITY, AND INDUCTION.

COMMENT On Nov 13, 2007 this sequence version replaced gi:74718013.
 [FUNCTION] Inhibits cell growth by regulating the FRAP1 pathway upstream of the TSC1-TSC2 complex and downstream of AKT1. Promotes neuronal cell death.
 [SUBCELLULAR LOCATION] Cytoplasm.
 [TISSUE SPECIFICITY] Broadly expressed, with lowest levels in brain, skeletal muscle and intestine. Up-regulated in substantia nigra neurons from Parkinson disease patients (at protein level).
 [INDUCTION] Up-regulated in fibroblasts upon ionizing radiation, via a TP53-dependent pathway. Up-regulated by TP63 in primary keratinocytes, and down-regulated during keratinocyte differentiation. Up-regulated upon DNA alkylation. Up-regulated by amyloid beta-peptide and retinoic acid. Up-regulated by hypoxia, via a PI3K and HIF1A-dependent but TP53/TP63-independent mechanism (at protein level).
 [SIMILARITY] Belongs to the DDIT4 family.

FEATURES

source Location/Qualifiers

1..232

/organism="Homo sapiens"

/db_xref="taxon:9606"

gene 1..232

/gene="DDIT4"

/note="synonyms: REDD1, RTP801"

Protein 1..232
 /gene="DDIT4"
 /product="DNA-damage-inducible transcript 4 protein"
Region 1..232
 /gene="DDIT4"
 /region_name="Mature chain"
 /experiment="experimental evidence, no additional details recorded"
 /note="DNA-damage-inducible transcript 4 protein.
 /FTId=PRO_0000307197."
Region 104..223
 /gene="DDIT4"
 /region_name="RTP801_C"
 /note="RTP801 C-terminal region. The members of this family are sequences similar to the C-terminal region of RTP801, the protein product of a hypoxia-inducible factor 1 (HIF-1)- responsive gene; pfam07809"
 /db_xref="CDD:71249"
Region 228
 /gene="DDIT4"
 /region_name="Conflict"
 /experiment="experimental evidence, no additional details recorded"
 /note="L -> P (in Ref. 4; CAB66603)."

ORIGIN

```

1 mpelwdrfss sstsssspsl prtpdpdrpp rsawgsatre egfdrstsls ssdcesldas
61 nsqfgpeedt ayldgvsldp felledpede hlcanlmql qeslaqarlg srrparllmp
121 sqivsavgke llrlaysepc glrgalldvc veggkschsv gqialdpslv ptfqltlvlr
181 ldsrlwpkiq glfssanspf lpgfsqsltl stgrfvikkk lysseqllie ec

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